Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	thermogenic protein	USPAT	ADJ	ON	2004/06/08 20:36

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New UPM (Update Code Maximum) field for more efficient patent
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                                                                                                                                                                      German (DE) application and patent publication number format
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                                                             "Ask CAS" for self-help around the clock
Source of Registration (SR) information in REGISTRY updated
                                                                                                                             A new search aid, the Company Name Thesaurus, available in
                                                                                                                                                                                                                                                                                                                                                                                                                         NLDB: New search and display fields available PROUSDDR now available on STN PROUSDDR: One FREE connect hour, per account, in both May
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FRANCEPAT now available on STN
Pharmaceutical Substances (PS) now available on STN
                                         Web Page URLs for STM Seminar Schedule - N. America
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AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
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=> index biosci

FILE 'DRUGMONG' ACCESS NOT AUTHORIZED COST IN U.S. DOLLARS

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SESSION

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOGRAMERRER, BIOGSIS, BIOTECHABS, BIOTECHAB, BIOTECHAB, BOTECHAB, CANCERLIT, CAPLUS, CEABA-VYE, CEN, CIN, CONSCII, CROPB, CROPE, CROPE, DISSABS, DDFW, DGENE, DRUGGN, DRUGMONOGZ, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

70 FILES IN THE FILE LIST IN STNINDEX

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=> s (thermogenic (w) protein) (p) (skunk (w) cabbage) 0* FILE ADISNEWS

0* FILE BIOCOMMERCE

FILE BIOTECHABS FILE BIOTECHDS *0

LE BIOTECHNO

0* FILE CEABA-VTB 0* FILE CIN

25 FILES SEARCHED.

FILE ESBIOBASE FILE FEDRIP *

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FILE NUTRACEUT

PHARMAML FILE PASCAL FILE PHARMA

62 FILES SEARCHED.

70 FILES SEARCHED IN STNINDEX 1 FILES HAVE ONE OR MORE ANSWERS,

L1 QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

SESSION 1.35 SINCE FILE ENTRY COST IN U.S. DOLLARS => file hits

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FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004 COPYRIGHT (C) 2004 IFI CLAIMS(R) Patent Services (IFI)

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FILE COVERS 1950 TO PATENT PUBLICATION DATE: 3 Jun 2004 (20640603/PD)

FILE LAST UPDATED: 4 Jun 2004 (20040604/ED) HIGHEST GRANTED PATENT NUMBER: US2004087609

HIGHEST APPLICATION PUBLICATION NUMBER: US2004107471 UNITERM INDEXING IS AVAILABLE IN THE IFIUDB FILE UNITERM INDEXING LAST UPDATED: 27 May 2004 (20040527/UP)

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IFIPAT has been reloaded (12/21/2003). See HELP RLOAD for details.
INDEXING CURRENT THROUGH PAT PUB DATE: 25 Nov 2003 (20031125/PD)
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alignment is indicated by a dash (-). The alignment was made using a CLUSTAL W program. The characteristic domains of energy transfer proteins typical of mitochondria are surrounded by a square. The shaded bars (I-VI) above the upper sequence show estimated transmembrane domains. Fig. 4 shows a hydrophobic plot of SfuCPA. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TMI to TMS. FIG. 6 shows a hydrophobic plot of SfUCPB. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are 8 Figure (s).

10 Figure (s).

11 Shows the change of the temperature of the spadix in skunk cabbage and that of ambient temperature with a lapse of time.

12 Shows the results of northern blotting, indicating the expression profile of SIUCPa (A) and SIUCPb (B) in the spadix and leaf of skunk cabbage at room temperature (RI) and during cold treatment (4 degrees C for 3 days). The lower figures respectively show the results of ethidium bromide staining of non-decomposed RNA. Fig. 3 compares the alignment of amino acid sequences of SfUCPA and SfUCPB, together with potato UCP (StUCP), Arabidopsis UCP (ALPUMP) and human UCP. The asterisk (*) attached under the sequences indicate the same amino acid sequence, and the dot (.) indicates the conservative change in all of the sequences. The boldface indicates the same sequence between SfUCPA and SfUCPB. The gap introduced to optimize the sequence FIG. 5 shows a diagrammatic illustration of SfUCPA topology in the Unassigned Or Assigned To Individual (68000) WENDEROTH, LIND & PONACK, L.L.P., 2033 K STREET N. W., SUITE 800, WASHINGTON, DC, 20006-1021, US 20030929 20000612 Section 371 PCT Filing UNKNOWN 20020123 DIVISION 1 (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE) COPYRIGHT 2004 IFI on STN Utility; Patent Application - First Publication 10560887 IFIPAT; IFIUDB; IFICDB PLANT THERMOGENIC GENES AND PROTEINS 19990614 20040408 A1 20040408 Ito; Kikukatsu, Iwate, JP mitochondria membrane. ANSWER 1 OF 1 IFIPAT 64 THERMOGENIC 65668 PROTEIN Ito Kikukatsu (JP) 450 CABBAGE US 2004068105 US 2003-671628 WO 2000-JP3806 US 2002-9962 JP 1999-167439 US 2004068105 37 SKUNK APPLICATION => d 12 bib ab CHEMICAL CLMN PI AI RLI L2 AN TI INF IN PAF PAF 17

indicated by TM1 to TM4 and TM5

FIG. 7 shows a diagrammatic illustration of SfUCPB topology in the mitochondria membrane. FIG. 8 shows the results of in vitro translation using respective CDNAs of

molecular translated artificial product synthesized from a small ORF. Th inventions of his application include thermogenic genes named SfUCPa and SfUCPb which are derived from skunk cabbage. CDNA of each gene comprises the base sequence SEQ ID NO: 1 and 3, respectively. Thermogenic proteins, SfUCPA and SfUCPB, are expressed from genes SfUCPa and SfUCPb, comprises the amino acid sequence of SEQ ID NO: 2 and 4. the genes SfUCPa and SfUCPb as templates. () indicates a control, S a sense RNA, and AS an antisense RNA. The asterisk (*) indicates a non-specific product and the empty circle denotes the position of a low

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(FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSTRINESS, BIOCOMMERCE, BIOSTS, BIOTOCHARD, BIOTOCHAGO, GABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CTN, CONFSCI, CROPE, CIOPU, DISSABS, DDFB, DDFD, DGENE, DNGB, DRUGMONG2, ... ENTERED AT 20:39:16 ON 08 JUN

SEA (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE) QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE) FILE BIOCOMMERCE FILE BIOTECHABS FILE BIOTECHNO FILE CEABA-VTB FILE ESBIOBASE FILE BIOTECHDS NUTRACEUT FILE ADISNEWS MEDICONF FILE PASCAL FILE PHARMAML FILE FEDRIP FOREGE IFIPAT FROSTI FILE KOSMET FILE MEDICO FOMAD FILE NTIS FILE FILE FILE FILE FILE FILE

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

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SESSION 7.26 TOTAL SINCE FILE 5.91 ENTRY COST IN U.S. DOLLARS FULL ESTIMATED COST => log y

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OM protein - protein search, using sw model

May 18, 2004, 11:11:47; Search time 48.3433 Seconds (without alignments) 1566.356 Million cell updates/sec Run on:

US-10-009-962-4 1382 1 MGDHGPRIEISFAGSSRAAF.....VIMFLTLEQVKKFFIKEVPN 268 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
No.	Score	Match 1	Match Length DB	Π	Description	
1	1382	100.0	268 4	AAB73298	Aab73298 SfUCPa de	
7	1344.5	97.3	303 4	AAB73297	Aab73297 SfUCPa de	
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4	1031		305 3	AAG05380	Aag05380 Arabidops	
5	1031		305 3	AAG48337	Aag48337 Arabidops	
9	1024.5		318 3	AAG48300	Aag48300 Arabidops	
7	712.5		212 3	AAG41404	Aag41404 Arabidops	
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ALIGNMENTS

SfUCPa derived exothermicity relating gene; diabetes; obesity; exothermic material; low temperature resistant plant. SfUCPa derived exothermicity relating gene protein #2. AAB73298 standard; protein; 268 AA. 29-MAY-2001 (first entry) AAB73298; RESULT 1 AAB73298

Symplocarpus foetidus.

JP2000354489-A.

61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 GPNIARNAIINAAELASYDQVKQMKSRMMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPN 240 181 GPNIARNAIINAAELASYDQVKQMKSRMMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPN 240 GIVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 121 AGLTTGALAIIVANPTDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL 180 9 1 MGDHGPRIEISFAGSSRAAFAACFAELCTIPLDIAKVRLQLQKKAVIGDVVALPKYRGML 60 of (SfUCPa) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment diabetes and obesity. The encoded protein is useful as exothermic 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML ξ The present sequence is a protein encoded by a Symplocarpus foetidus Exothermicity relating genes and proteins, useful in the treatment ; 0 Length 268; Indels 100.0%; Score 1382; DB 4; 100.0%; Pred. No. 8.5e-138; tive 0; Mismatches 0; FGRLGSWNVIMFLTLEQVKKFFIKEVPN 268 FGRLGSWNVIMFLTLEQVKKFFIKEVPN 268 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. Claim 4; Page 10-11; 15pp; Japanese. AAB73297 standard; protein; 303 99JP-00167439. 99JP-00167439 materials for industrial use 29-MAY-2001 (first entry) 268; Conservative diabetes and obesity. 2001-260368/27. Similarity N-PSDB; AAF77826. Sequence 268 AA; 14-JUN-1999; 14-JUN-1999; 26-DEC-2000. AAB73297; 19 181 241 Query Match Local Matches RESULT 2 AAB73297 g ò В à g ò g ò

(SfUCPa) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment of diabetes and obesity. The encoded protein is useful as exothermic materials for industrial use

The present sequence is a protein encoded by a Symplocarpus foetidus

Claim 3; Page 7-8; 15pp; Japanese.

diabetes and obesity.

Exothermicity relating genes and proteins, useful in the treatment of

(KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN.

2001-260368/27.

N-PSDB; AAF77825.

99JP-00167439. 99JP-00167439.

14-JUN-1999; 14-JUN-1999;

26-DEC-2000.

obesity;

SfUCPa derived exothermicity relating gene; diabetes; exothermic material; low temperature resistant plant. SfUCPa derived exothermicity relating gene protein #1.

Symplocarpus foetidus.

JP2000354489-A.

205 61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 121 AGLTTGALAIIVANPTDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL 180 -- MK 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 1 MGDHGPRIEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 61 GTVATIAREEGLSALWKGIVPCLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 1; Indels 35; Gaps Length 303; DB 4; Score 1344.5; DB 4; Pred. No. 9.7e-134; 0; Mismatches 1; 181 GPNIARNAIINAAELASYDQVKQ-97.3%; 88.1%; Matches 267; Conservative Local Similarity Sequence 303 AA; Query Match à g ò Db ò 엽 à g 8

266 VPN 268 ð

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Search completed: May 18, 2004, 11:18:52 Job time : 49.3433 secs

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OM protein - protein search, using sw model

May 18, 2004, 11:16:57; Search time 15.4886 Seconds (without alignments) 893.286 Million cell updates/sec Run on:

Title:
US-10-009-962-4
Perfect score: 1382
Sequence: 1 MGDHGPRIEISFAGSSRAAF......VIMFLILEQVKKFFIKEVPN 268

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 segs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

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6. /cgn2 6/ptodata/2/iaa/Parrus_COMB.pep:*

6. /cgn2 6/ptodata/2/iaa/Parrus_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	, Appl
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Description	Sequence 4,	Seguence	Seguence 4,	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence 51, Appl
ID	US-08-937-466-4	US-09-172-528-4	US-09-318-199-4	US-09-503-579-4	US-09-743-847-4	US-10-001-051B-2	US-08-937-466-2	US-09-172-528-2	US-09-318-199-2	US-09-503-579-2	US-08-518-878B-51
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Query	43.1	43.1	43.1	43.1	43.0	43.0	42.9	42.9	42.9	42.9	42.8
Score	595	595	595	595	594	594	593	593	593	593	592
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12	13	14	15				19	20	21	22	23	24	52	56	27	28	29		31		33		35	36	37	38	39	40	41	42	43	44	45

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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:20:53; Search time 36.6095 Seconds

Title:

US-10-009-962-4

Perfect score: 1382
Sequence: 1382
Sequence: 1382
Sequence: 1385
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1145568 seqs, 278261457 residues
Total number of hits satisfying chosen parameters: 1145568
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Inisting first 45 summaries
Database: Published Applications AA:*

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2: /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
4. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
7. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
7. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
7. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
7. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*
7. /cgn2_6/prodata/l/pubpaa/PCT_NEW_PUB.pep:*

Published Applications_AA:*

| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description

Sequence 4, Appli	equence 2,	equence 5,	equence 23	equence 6	6	equence 20	٦,	equence 8,	ce 1	ω	equence 2	e e		ednence 3	4	9	Sequence 2, Appli	7	7	o,	equence 3	H	equence 2	equence 2	CA.	ednence 8	œ	ednence 1	equence 3	-	ednence 8	Sequence 90, Appl	quence 4,	ednence e	Sequence 2	Seguence 2	Sequence 2	Seguence 52234, A	equence 406,	Sequence 126, App	Seguence 126, App	ý,	12	126,
.2 US-10-671-628-4	2 US-10-671-628-	2 US-10-671-62	S-10-424-599-2376	2 US-10-425-114-66317	2 US-10-671-628-6	2 US-10-424-599-	US-09-884-814	-09-884-814-	2 US-10-336-472	2 US-10-671-628-	3 US-10-00	4 US-10-270-861-3	14 US-10-265-689-1	-10-197-019-	US-09-823-886A	-884-814-	US-09-734-1	-09-826-507-	US-09-808-457-	L2 US-10-671-628-9	US-10-270-861-3	2 US-10-336-472-13	US-10-424-59	2 US-10-037-417-2	0 US-09-823-88	2 US-10-037-417-8	US-10-037-417-8	2 US-10-671-628-7	4 US-10-270-861-3	US-10-037-417-	2 US-10-037-417-8	US-10-037-417-9	US-09-808-45	0 US-09-823-886A-6	2 US-10-424-599-21761	2 US-10-424-599-2760	US-10-424-599-27609	2 US-10-425-114-5223	0 US-09-946-374-40	12 US-10-063-745-126	US-10-063-512-12	US-10-063-513-1	12 US-10-063-515-126	2 US-10-063-549-12
1			305										309	309	314	309	312	312	312	312								307	307	307	306	306	275	284	300	317	317				323	323	323	323
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	~ ~	m	4	ינו	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40		42	43	44	45

TITLE OF INVENTION: Plant Thermogenic Genes and Proteins FILE REFERENCE: 2003-1386A/WMV/00653
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/671,628
PRIOR FILING DATE: 2003-09-29
PRIOR FILING DATE: 2003-09-29
PRIOR FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: PCT/JP00/03806
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0

LENGTH: 268

, SEQ ID NO 4

ALIGNMENTS

RESULT 1
US-10-671-628-4
Sequence 4, Application US/10671628
Publication No. US2040068105A1
GENERAL INPERMITION:
APPLICANT: ITO, Kikukatsu

°, 61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 61 GTVATIAREBGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 181 GFNIARNAIINAAELASYDQVKQMKSRWMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPN 240 121 AGLTTGALAIIVANPTDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL 180 181 GPNIARNAIINAAELASYDQVKQMKSRMMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPN 240 Query Match 100.0%; Score 1382; DB 12; Length 268; Best Local Similarity 100.0%; Pred. No. 1.1e-136; Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps RESULT 2
US-10-671-628-2
; Septication US/10671628
; Publication No. US20040068105A1
; GENERAL INFORMATION:
; APPLICANT: ITO, KIKURATSU
; TITLE OF INTENTION: Plant Thermogenic Genes and Proteins; FILE REFRENCE: 2003-1386A/WWC/00653
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-01-23
; RIOR FILING DATE: 2002-01-23
; RIOR PLILORION NUMBER: PCT/JP00/03806 241 FGRLGSWNVIMFLTLEQVKKFFIKEVPN 268 241 FGRLGSWNVIMFLTLEQVKKFFIKEVPN 268 TYPE: PRT ORGANISM: Symplocarpus foetidus US-10-671-628-4 ò Ωp ô g ò ΩD ò g ઠે

61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 121 AGLTTGALAIIVANPTDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL 180 181 GPNIARNAIINAAELASYDQVKQ-----MK 205 206 SRMMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 265 241 SRWMGDSAYKSTFDCFIKTLKANDGLLAFYKGFIPNFGRLGSWNVIMFLTLEGVKKFFIKE 300 61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 9 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 35; Gaps Query Match 97.3%; Score 1344.5; DB 12; Length 303; Best Local Similarity 88.1%; Pred. No. 1.1e-132; Matches 267; Conservative 0; Mismatches 1; Indels 35; Search completed: May 18, 2004, 11:30:31 Job time : 36.6095 secs PRIOR APPLICATION NUMBER: JP11-167439 PRIOR FILING DATE: 1999-06-14 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN Ver. 2.0 , ORGANISM: Symplocarpus foetidus US-10-671-628-2 Query Match Best Local Similarity 266 VPN 268 301 VPN 303 LENGTH: 303 SEQ ID NO 2 TYPE: PRT ò g ò g ò g ò q ò g

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OM protein - protein search, using sw model

Run on:

May 18, 2004, 11:16:07; Search time 13.6112 Seconds

(without alignments)
1893.978 Million cell updates/sec
1893.978 Million cell updates/sec
1893.978 Million cell updates/sec
Sequence:
1893.978 Million cell updates/sec

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

uncoupling protein mitochondrial unco uncoupling protein uncoupling protein F7A19.22 protein hypothetical prote uncoupling protein Description SUMMARIES T52024 JC5522 G01858 S34268 A26294 A31106 A32446 T07793 T47570 H86274 D84613 T05577 Ω Query Match Length DB 23.75 27.55 27.55 2.75 2.05 2.05 2.05 4.05 4.05 504.5 503.5 423.5 421.5 Score 1049 1040 592 Ñ

hypothetical prote		hypothetical prote		2-oxoglutarate/mal	2-oxoglutarate/mal	oxoglutarate/malat	2-oxoglutarate car	oxoglutarate/malat	probable dicarboxy	hypothetical prote	probable oxaloacet	mitochondrial unco	probable 2-oxoglut	probable carrier p		hypothetical prote	protein K11H3.3 [i	hypothetical prote	ADP, ATP carrier pr	transpor	probable membrane	peroxisomal Ca-dep	hypothetical prote	ADP, ATP carrier pr	hypothetical prote		ADP, ATP carrier pr	uncoupling protein	citrate transport	envelope protein L	hypothetical prote
T15253	JC7553	T25459	S65040	S65042	A36305	T07405	A56650	\$44091	149628	\$51351	T37603	\$25357	T51899	\$57116	A46595	T48171	H88567	T48156	S51132	G01789	S48451	T49871	116533	XWBO	751158	T15206	343646	S16082	\$44554	109109	123207
7	7	7	61	~	U	W	N	7	7	N	7	(7)	7	N	(1)	N	N	7	7	~	N	N	C)	Н	2	7	N	N	~	7	7
343	325	323	302	302	314	297	314	290	282	298	320	324	331	322	311	415	312	309	301	311	373	479	702	298	381	300	298	6	299	358	313
29.7	29.6	26.0	24.9		24.2	24.0	23.5	23.0	21.1	19.9	19.9	19.8	19.5	19.3	17.9	17.8	17.5	17.0	16.8	16.8	16.4	16.4	16.2	16.2	16.2	16.0	15.7	15.6	15.6	15.4	15.3
410.5	409.5	360	344	338	334.5	331	324.5	317.5	291.5	275	274.5	273.5	270	266.5	247.5		241.5	235.5	232.5	232.5	226.5	226		223.5	223.5	221	217.5		215.5	212.5	211.5
14	15	16	17	18	6⊺	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 T07793

C; Keywords: mitochondrion

	7	09	63	120	123	180	183	205	243		
	Gaps	KYRGML	KYRGLL	LSKKIL	LSKKIL	ALWIGL	ALWIGI	M K	PVDVVK	KF 261	 KF 299
. 90	36;	DWALP	GLALP)	FVGDIP	I I I I I	KKEGLG	KQEGVRJ		AVCIGS	FLEQVKI	rleqaki
81.1%; Score 1121; DB 2; Length 306; 73.0%; Pred No. 46.87.	Indels	2 GDHGPRIEISFAG-SSRAAFAACFAELCTIPLDIAKVRLQLQKKAVTGDVVALPKYRGML	GDHGGKSDISFAGIFASSAFAACFAEACTLPLDTAKVRLQLQKKAVBGDGLALPKYRGLL 63	61 GTVATIAREGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120	GTVGTIAKEEGIASLWKGIVPGLHRQCIYGGLRIGMYEPVKNLYVGKDHVGDVPLSKKIL	121 AGLTIGALAIIVANPTDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL	124 AALITGALGITIANPIDLVKVRLQAEGKLPAGVPRRYSGALNAYSTIVKQEGVRALWIGL 183	181 GPNIARNAIINAABLASYDQVKQ		206 SRMMGDSAYKSTFDCFIKTLKUNGPLAFYKGFIFNFGRLGSWNVIMFLTLEQVKKF 261	SRWMGDSAYKNTLDCFVKTLKNDGPLAFYKGFIPNFGRLGSWNVIMFLTLEQAKKF
DB 2;	18;	IAKVRLO	TAKVRLO	IGLYEPV	IGMYEPV	PRRYSGA	PRRYSGA		NVVTHLI	PNFGRLG	PNFGRLG
Score 1121; DB Dred No. 46,87.	26; Mismatches	CTIPLD	ACTLPLD	CLFGGLR	LIYGGLR	SKLPPGV	3KLPAGV		RIPGFTD	AFYKGFI	4FYKGFI
Score	6. Misi	FAACFAE	FAACFAE	VPGLHRQ	VPGLHRQ	KVRLQSE	KVRLQAE	OVKQ-	OVKEAVL)	LKNDGPL	LKNDGPL
81.18;	,	G-SSRAA	GIFASSA	SALWKGI	ASLWKGI.	ANPTDLV	ANPTOLV	SPNIARNAI INAAELASYDQVKQ	AELASYD	FDCFIKE	LDCFVKT
	servat	TEISFA	CSDISFA	REEGL	AKEEGI	SALAIIV	SALGITI	WALINA	RNALINA	SAYKST	SAYKNT
, E	6; CO	GDHGPI	GDHGG	GTVAT		AGLIT	AALTT	GPNIA	GPNIG	SRMMGI	
atch	21	N	₫	61	64	121	124	181	184	206	244
Query Match Rest Local Similarity	Matches 216; Conservative	ςλ	QQ	ςλ	Db	à	Db	ò	Db	٥y	ДQ
		Ū	1	Ū	н	J	ш	J	н	J	ш

Search completed: May 18, 2004, 11:21:31 Job time : 14.6112 secs

GenCore version 5.1.6 Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 18, 2004, 11:12:22 ; Search time 9.38704 Seconds (without alignments) 1486.603 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-009-962-4 1382 1 MGDHGPRIEISFAGSSRAAF......VIMFLTLEQVKKFFIKEVPN 268

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	601	43.5		-	UCP2 CYPCA	Q9w725 cyprinus ca
7	600.5	43.5		Н	UCP3 BOVIN	077792 bos taurus
m	597.5	43.2	311	٦	UCP3 CANFA	Q9n2i9 canis famil
4	595	43.1		н	UCP3 MOUSE	
ហ	595	43.1		Н	UCP2 MOUSE	P70406 mus musculu
Ψ	595	43.1		Н	UCP2 BRARE	Q9w720 brachydanio
7	594	43.0		н	UCP2 HUMAN	P55851 homo sapien
60	593	42.9		٦	UCP3 RAT	P56499 rattus norv
đΛ	593	42.9		٦	UCP2 PIG	097562 sus scrofa
10	592	42.8		Н	UCP2 RAT	P56500 rattus norv
11	592	42.8		н	UCP3 HUMAN	P55916 homo sapien
12	587	42.5		٦	UCP2 CANFA	Q9n2jl canis famil
13	583	42.2		H	UCP3_PIG	097649 sus scrofa
14	541	39.1		Н	UCP1 HUMAN	P25874 homo sapien
15	518	37.5		н	UCPL MESAU	P04575 mesocricetu
16	518	37.5	306	٦	UCP1_RAT	P04633 rattus norv
17	516	37.3	306	Н	UCP1 MOUSE	P12242 mus musculu

18	509.5	36.9	306	-	UCP1 RABIT	P14271 C	oryctolagus
19	503.5	36.4	288	Н	UCP1 BOVIN	P10861 b	bos taurus
20	436	31.5	323	Н	UCP4_HUMAN		homo sapien
21	410.5	29.7	325	Н	UCPS HUMAN	095258 h	homo sapien
22	406.5	29.4	325	+	UCP5 MOUSE	109z2b2 π	mus musculu
23	ø	26.5	287	-1	DIC HUMAN	Q9ubx3 h	homo sapien
24	351.5	25.4	287	Н	DIC_MOUSE	± 8pzb6ō	mus musculu
25	334.5	24.2	313	П	MZOM BOVIN	P22292 b	bos taurus
56	333.5	24.1	313	н	M2OM_MOUSE	09cr62 m	mus musculu
27	324.5	23.5	313	Н	M2OM HUMAN		homo sapien
28	318.5	23.0	313	M	M2OM RAT		rattus norv
29	273.5	19.8	324	Н	OAC1_YEAST		saccharomyc
30	266.5	19.3	322	ч	SFC1_YEAST	P33303 8	saccharomyc
31	247.5	17.9	311	m	TXTP_RAT		rattus norv
32	241.5	17.5	312	٦	TXTP CAEEL		caenorhabdi
33	232.5	16.8	311	Н	TXTP_HUMAN		homo sapien
34	231.5	16.8	311	Н	TXTP_BOVIN		bos taurus
35	226.5	16.4	373	Н	YIA6_YEAST		saccharomyc
36	226	16.4	675	Н	CMC2_HUMAN		homo sapien
37	224.5	16.2	702	H	CMC1_CAEEL		caenorhabdi
38	224	16.2	299	П	ODC_HUMAN		homo sapien
39	223.5	16.2	297	Н	ADT1_BOVIN		bos taurus
40	222.5	16.1	316	,-1	MFTC MOUSE	n 85md80	mus musculu
41	222	16.1	300	Н	MCAT_ARATH	693xm7	arabidopsis
42	220	15.9	919	~	CMC2_MOUSE	09qxx4 n	mns mnscnjn
43	219.5	15.9	678	Н	CMC1_HUMAN		homo sapien
44	219	15.8	298	П	ODC_RAT	Q99jd3 1	rattus norv
45	217.5	15.7	298	Н	ADT3_BOVIN		bos taurus
•					((((((((((((((((((((

Search completed: May 18, 2004, 11:19:24 Job time : 10.387 secs

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May 18, 2004, 11:11:47; Search time 54.6567 Seconds (without alignments) 1566.356 Million cell updates/sec Run on:

OM protein - protein search, using sw model

US-10-009-962-2 1561 1 MGDHGPRTEISFAGSSRAAF.....VIMFLTLEQVKKFFIKEVPN 303 Title: Perfect score: Sequence:

1586107 seqs, 282547505 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:*

1. geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
6: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab73297 SfUCPa de	Aab73298 SfUCPa de	Aag41403 Arabidops	Aag05380 Arabidops	Aag48337 Arabidops	Aag48300 Arabidops	Aag41404 Arabidops	Aag41405 Arabidops	Aaw81595 Mouse unc
Ð	AAB73297	AAB73298	AAG41403	AAG05380	AAG48337	AAG48300	AAG41404	AAG41405	AAW81595
ВВ	4	4	m	m	m	m	m	m	~
% Query Match Length DB	303	268	306	305	305	318	212	177	308
% Query Match	100.0				77.3			47.9	43.9
Score	1561 100.0 303	1344.5	1232.5	1206.5	1206.5	1190	896	748	685.5
Result No.		(7)	m	4	S	9	7	80	Q

10	685.5	43.9		0	328	Aaw88280	Mouse unc
11		m			983	י מ	Mouse unc
12		m d			AAW85117	A4W0511/	Murine mi
m ;		4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4			AA1/455	· ~	
	685 700 700 700	4. 4. 2. 4. 2. 4.	208	* ~	AAY29834	983	
16	683.5	i m			AAW85116	111	-
17		m			AAY77452	15	
18		m			AAE04729	75	5.
19	682.5	43.7			AAW81596	9	
20		m			AAW81588	00 1	Proce
21		m			AAW81587		
22		ന			AAWGYLDG	A4W69166	110001
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24	77.	ካ ເ			AACSSOI 2DES4389	AGE54389	Rat Pr
57.0		າເ			ADD-4-109	7 .	Ниша
56	0. U. U.	4. c.			AMMOSSICA	. 6	Human
7 0		ባ ሶ			NAME OF THE PARTY	Aaw85667	Human
2 0		າຕ			AAW88279	827	Human
6 6		۱ ۳			AAY31904	Aay31904	Human
3 5		4 4 3 5			AAY54600	Aay54600	Amino
3.5		ຸຕ			AAY44253	425	Нишап
33		43.3			AAB74296	•	Human UCP
34		(س			AAE04298	•	Human
35		L.)			AAB68050	305	Amino
36		L.J	312		ABB81610	191	UCP3L
37		43.3	312		AAE19348	1934	Human
38	75	C.I	312		ADE54391	439	Human
39	74	43.2	309	~	AAY28351	m	UCP2 a
40	74	(,,	309		AAY31903	190	Human
41	74	.,	309		AAY44292	44 T	
4.2	74	.,,	309		AAY45002	900	Tarn
43	4	43.2	309		AAY72342	ay7234	Human
44	-	43.2	314	4	AAU09077	907	7
4.5	672.5	43.1	309	N	AAW24000	Aaw24000	псощотеге
					STNERMOTIA		
RESULT	-						
AAB7329	- 6						
ID AA	73297	standard;	protein	ď	303 AA.		
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DE SI	rucka der	derived exor	ner mit	1	reracting gene process		
	fUCPa der	ived	按	it.	relating gene; diabetes	, obesity	
	exothermic	materı	al; low)	S CALL		
	Symplocarpus	foet	idus.				
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73	6-DEC-2000	0.					
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ö 61 GTVATIAREBGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 SRMMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 300 241 SRMMGDSAYKSTEDCFIKTLKAVDGLLAFYKGFIPNFGRLGSWAVIMFLTLEQVKKFFIKE 300 61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 121 AGLITGALAIIVANPIDLVKVRLQSEGKLPPGVPRRYSGALNAYSTIVKKEGLGALWTGL 180 GPNIARNAIINAAELASYDQVKQTILKLPGFSDNIFTHILAGLGAGFFAVCIGSPVDVMK 240 The present sequence is a protein encoded by a Symplocarpus foetidus (SfUCPa) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment of diabetes and obesity. The encoded protein is useful as exothermic materials for industrial use 9 9 1 MGDHGPRIEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML Gaps 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML Exothermicity relating genes and proteins, useful in the treatment of ö 100.0%; Score 1561; DB 4; Length 303; 100.0%; Pred. No. 6.5e-151; ive 0; Mismatches 0; Indels 0; (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN. AAB73298 standard; protein; 268 AA. Claim 3; Page 7-8; 15pp; Japanese. 99JP-00167439. 99JP-00167439. Best Local Similarity 100. Matches 303; Conservative diabetes and obesity. WPI; 2001-260368/27. VPN 303 VPN 303 N-PSDB; AAF77825 Sequence 303 AA; 14-JUN-1999; 14-JUN-1999; 181 301 AAB73298; Query Match AAB73298 ID AAB7 XX AC AAB7 XX RESULT 2 g ò g ઠે qq ò g ò ò g ò

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61 GTVATIAREEGLSALWKGIVPGLHRQCLFGCLRIGLYBPVKSFYVGDNFVGDIPLSKKIL 120
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                                                                                                                                                                                                                                                               KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN.
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88.1%;
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exothermicity relating gene; diabetes; obesity;

exothermic material; low temperature resistant plant

SfucPa derived

Symplocarpus foetidus.

SfUCPa derived exothermicity relating gene protein #2.

(first entry)

29-MAY-2001

206 SRMMGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 265

301 VPN 303 à

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Search completed: May 18, 2004, 11:18:51 Job time : 56.6567 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 18, 2004, 11:16:57 ; Search time 17.5114 Seconds (without alignments) 893.286 Million cell updates/sec Title:
US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHGPRTEISFAGSSRAAF.......VIMFLTLEQVKKFFIKEVPN 303 Run on:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 segs, 51625971 residues Searched: 389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

May 18, 2004, 11:20:53; Search time 41.3905 Seconds (without alignments) 2037.017 Million cell updates/sec Title: US-10-009-962-2
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SUMMARIES

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PRIOR FILING DATE: 2000-06-12
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.0

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> Sequence 2, Application US/10671628
> Publication No. US2040068105A1
> GENERAL INFORMATION:
> APPLICANT: ITO, Kikukatsu
> TILLE OF INVENTION: Plant Thermogenic Genes and Proteins
> FILE REFERENCE: 2003-13864/WMV/00553
> CURRENT APPLICATION NUMBER: US/10/671,628 RESULT 1 US-10-671-628-2

ALIGNMENTS

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Sequence 4, Application US/10671628

Sequence 4, Application US/10671628

Publication No. US20040068105A1

GENERAL INFORMATION:

APPLICANT: ITO, Kikukatsu

TITLE OF INVENTION: Plant Thermogenic Genes and Proteins

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; ORGANISM: Symplocarpus foetidus
US-10-671-628-2
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61 GTVATIAREBGLSALWKGIVPGLHRQCLFGGLRIGLXBPVKSFYVGDNFVGDIPLSKKIL 120 241 SRMMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 300 206 SRWAGDSAYKSTFDCFIKTLKNDGPLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 265 181 GPNIARNAIINAAELASYDQVKQTILKT.PGFSDNIFTHILAGLGAGFFAVCIGSPVDVMK 240 61 GTVATIAREEGLSALWKGIVPGLHRQCLFGGLRIGLYEPVKSFYVGDNFVGDIPLSKKIL 120 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 60 1; Indels 35; Gaps Ouery Match 86.1%; Score 1344.5; DB 12; Length 268; Best Local Similarity 88.1%; Pred. No. 2.3e-128; Matches 267; Conservative 0; Mismatches 1; Indels 35; PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION WOMBER: JP11-167439
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 268 Search completed: May 18, 2004, 11:30:31 Job time : 42.3905 secs ; TYPE: PRT ; ORGANISM: Symplocarpus foetidus US-10-671-628-4 266 VPN 268 301 VPN 303 g g OD ò ŏ g ò g õ à ò

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2004, 11:16:07; Search time 15.3888 Seconds (without alignments) 1893.978 Million cell updates/sec

Title:
Perfect score: 1561
Sequence: 1 MGDHGPRIEISFAGSSRAAF......VIMPLTLEQVKKFFIKEVPN 303

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 4
Listing first 4
Database : PIR_78:*
1: Dirl:*
3: pirs:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description 1 1294.5 82.9 306 2 T07793 uncoupling protein 3 1232.5 79.0 306 2 T52024 uncoupling protein 4 675.5 43.3 31.2 2 JC5222 uncoupling protein 5 591.5 37.4 307 2 G01858 uncoupling protein 6 591.5 37.4 307 2 G01858 uncoupling protein 7 589.5 37.8 306 2 A3106 uncoupling protein 9 583.5 37.4 307 2 S34.56 uncoupling protein 10 574 36.8 2 S36.3 uncoupling protein 11 520 33.3 313 2 D84613 incoupling protein 12 510 32.7 313 2 D84613 incoupling protein 13 508 32.5 30.6 2 H86274 rosesure 14 F7A15.22 protein 15 508 32.5 30.6 2 H86274 F7A15.22 protein	Result		Query				
1294.5 82.9 306 2 T07793 1233.5 79.0 306 2 T47570 675.5 43.3 312 2 UC5522 614.5 39.4 307 2 M5294 589.5 37.9 307 2 M5294 589.5 37.8 306 2 A31106 583.5 37.4 307 2 A5294 574 368 2 S0603 520 33.3 313 2 D04613 508 32.5 30.5 2 H86274	No.	Score	Match	Length	DB	DI .	Description
1222.5 79.0 306 2 T47570 1223.5 78.4 306 2 T52024 614.5 39.4 307 2 G01858 644.5 39.4 307 2 G01858 589.5 37.8 306 2 A31106 583.5 37.4 307 2 S34268 574 368 2 S3446 570 33.3 313 2 D94613 508 32.5 30.5 2 H86274	1	1294.5	82.9		7	T07793	uncoupling protein
1223.5 78.4 306 2 T22024 675.5 43.3 312 2 UC5522 614.5 37.9 307 2 G01858 591.5 37.9 307 2 A26294 589.5 37.8 306 2 A31106 579 37.1 306 2 A3246 579 37.3 313 2 D84613 520 33.3 313 2 D84613 508 32.5 30.5 2 H86274	7	1232.5	79.0	306	7	T47570	uncoupling protein
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614.5 39.4 307 2 G01858 589.5 37.9 307 2 A26294 589.5 37.8 306 2 A31026 583.5 37.4 307 2 S34268 579 37.1 306 2 A32446 574 36.8 288 2 S03603 520 33.3 313 2 D84613 508 32.5 305 2 H86274	4	675.5	43.3	312	7	JC5522	uncoupling protein
591.5 37.9 307 2 A26294 583.5 37.8 306 2 A31106 583.5 37.4 306 2 S3268 579 37.1 306 2 A32446 574 36.8 2 S3603 520 33.3 313 2 D84613 508 32.5 30.5 2 H86274	Ŋ	614.5		307	7	G01858	uncoupling protein
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583.5 37.4 307 2 S34268 579 37.1 306 2 A32446 574 36.8 288 2 S02603 520 33.3 313 2 D84613 510 32.7 313 2 T05577 508 32.5 305 2 H86274	7	589.5		306	7	A31106	mitochondrial unco
579 37.1 306 2 A32446 574 36.8 288 2 S03603 520 33.3 313 2 T05577 510 32.7 313 2 T05577 508 32.5 305 2 H86274	ω	583.5	37.4	307	7	S34268	uncoupling protein
574 36.8 288 2 SO3603 520 33.3 313 2 D84613 510 32.7 313 2 D8577 508 32.5 305 2 H86274	σ	579	37.1		7	A32446	uncoupling protein
33.3 313 2 D84613 1 32.7 313 2 T05577 1 32.5 305 2 H86274	10	574	36.8		7	503603	uncoupling protein
32.7 313 2 T05577 32.5 305 2 H86274	11	520	33.3		7	D84613	hypothetical prote
32.5 305 2 H86274	12	510	32.7		(1	T05577	uncoupling protein
	13	508	32.5		(7)	H86274	F7A19.22 protein -

hypothetical prote	brain mitochondria	hypothetical prote	2-oxoglutarate/mal	2-oxoglutarate car	oxoglutarate/malat	probable dicarboxy	oxoglutarate/malat	2-oxoglutarate/mal	2-oxoglutarate/mal	hypothetical prote	probable oxaloacet		probable 2-oxoglut			ical pro	protein KllH3.3 [i	ADP, ATP carrier pr	hypothetical prote	peroxisomal Ca-dep	citrate transporte	tricarboxylate tra	citrate transport	hypothetical prote	probable membrane	probable membrane	probable tricarbox	_	_	_	hypothetical prote	
T15253	JC7553	10	A36305	A56650	S44091	T49628	T07405	865040	S65042	S51351	T37603	S25357	T51899	S57116	T48156	T48171	H88567	851132	T15206	T49871	G01789	A46595	S44554	T51158	S48451	869050	T37992	T16533	T23207	T25850	T45934	ALIGNMENTS
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34	325	323	314	31,	29(28.	297	30.	30:	29	320	32	331	32.	309	415	312	301	300	47	311	311	299	38	37	310	29	70	31	31	35	
30.9	30.8	28.3	26.9	26.2	24.5	24.3	23.2	23.0	22.6	21.6	20.6	20.4	20.4	19.3	17.7	17.6	17.5	17.0	16.6	16.6	16.5	16.5	16.3	16.1	16.1	15.8	15.7	15.7	15.6	15.6	15.5	
483	481	441.5	420	409	382	379	361.5	58	353.5	337.5	321	319	318.5	302	277	275	7	266	258.5	258.5	257	257	254	252	251	246.5	45	4	244	244	241.5	
14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29	30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	45	

RESULT 1

uncoupling protein (clone StUCP7), mitochonrial - potato C;Species: Solanum tuberosum (potato) (c;Species: Solanum tuberosum (potato) (c;Species: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000 C;Accession: 107793 (c;Accession: 10779) (c;Acc

A;Residues: 1.306 <LALD A;Cross-references: EMBL:Y11220; NID:g2398828; PIDN:CAA72107.1; PID:g2398829 A;Experimental source: cv. Desiree A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

A;Genome: nuclear A;Genome: nuclear C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: mitochondrion

DB 2; Length 306 82.9%; Score 1294.5; Query Match

181 GPNIARNAIINAAELASYDQVKQTILKLPGFSDNIFTHILAGLGAGFFAVCIGSPVDVMK 240 9 63 2 GDHGPRIEISFAG-SSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 241 SRMMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKF 296 244 SRWMGDSAYROTIDGFVKTLKNDGPLAFYKGFIPNFGRLGSWNVIMFLILEQAKKF 299 1; Gaps Best Local Similarity 81.4%; Pred. No. 1.1e-95; Matches 241; Conservative 33; Mismatches 21; Indels Search completed: May 18, 2004, 11:21:30 Job time : 16.3888 secs g g ò g ò δ g ò ò

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OM protein - protein search, using sw model

Run on: May 18, 2004, 11:12:22 ; Search time 10.613 Seconds
(without alignments)
1486.603 Million cell updates/sec

Title: US-10-009-962-2
Perfect score: 1561
Sequence: 1 MGDHGPRTEISFAGSSRAAF......VIMFLTLEQVKKFFIKEVPN 303

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Gapop 10.0 , Gapext 0.5 Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					1	
		υ¥P				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	685.5	43.9	308	-	UCP3 MOUSE	P56501 mus musculu
. 73	684	43.8	311	-	UCP3_BOVIN	077792 bos taurus
m	684	43.8	311	ч	UCP3 CANFA	Q9n2i9 canis famil
4	681.5	43.7	308	۲	UCP3 RAT	P56499 rattus norv
ហ	681.5	43.7	309	٦	UCP2_PIG	097562 sus scrofa
Ø	680.5	43.6	309	~	UCP2 MOUSE	P70406 mus musculu
7	679.5	43.5	310	Н	UCP2 CYPCA	Q9w725 cyprinus ca
60	677.5	43.4		ત	UCP2_RAT	P56500 rattus norv
σ	675.5	43.3		٦	UCP3 HUMAN	P55916 homo sapien
10	674.5	43.2		Н	UCP2 HUMAN	P55851 homo sapien
11	673.5	43.1		Н	UCP2 BRARE	Q9w720 brachydanio
12	669.5	42.9		m	UCP3 PIG	097649 sus scrofa.
13	667.5	42.8		П	UCP2 CANFA	Q9n2jl canis famil
14	613.5	39.3		-	UCP1 HUMAN	P25874 homo sapien
15	591.5	37.9		Н	UCP1 RAT	P04633 rattus norv
16	589.5	37.8	306	Т	UCP1 MOUSE	P12242 mus musculu
17	583.5	37.4		m	UCP1_MESAU	
1.8	579	37.1	306	Ч	UCP1 RABIT	P14271 oryctolagus

P10861 bos taurus	095847 homo sapien	095258 homo sapien	Q922b2 mus musculu	Q9ubx3 homo sapien	Q9qzd8 mus musculu	P22292 bos taurus	Q9cr62 mus musculu	Q02978 homo sapien	P97700 rattus norv	P32332 saccharomyc	P33303 saccharomyc	P34519 caenorhabdi	Q99jd3 rattus norv	Q93xm7 arabidopsis	Q8bmg8 mus musculu	Q9bqt8 homo sapien	Q9ujs0 homo sapien	Q9h2d1 homo sapien	Q9qxx4 mus musculu	P53007 homo sapien	P32089 rattus norv	Q95j75 macaca fasc	P38152 saccharomyc	P79110 bos taurus	075746 homo sapien	P40556 saccharomyc
1 UCP1 BOVIN	1 UCP4_HUMAN	1 UCPS HUMAN	1 UCP5 MOUSE	1 DIC HUMAN	1 DIC MOUSE	1 M20M_BOVIN	1 M2OM MOUSE	1 M2OM HUMAN	1 M2OM RAT	1 OAC1 YEAST	1 SFC1 YEAST	1 TXTP_CAEEL	1 ODC_RAT	1 MCAT ARATH	1 MFTC_MOUSE	1 ODC HUMAN	1 CMC2 HUMAN	1 MFTC HUMAN	1 CMC2 MOUSE	1 TXTP HUMAN	1 TXTP RAT	1 MFTC MACFA	1 TXTP_YEAST	1 TXTP BOVIN	1 CMC1_HUMAN	1 YIA6_YEAST
288	323 1	325	325	287	287	313	313	313	313	324	322	312	.862	300	316	299	675	315	929	311	311	315	299	311	678	373
36.8	33.6	30.8	30.6	28.7	27.5	26.9	26.8	26.2	25.6	20.4	19.3	17.5	17.5	17.0	16.9	16.9	16.9	16.6	16.5	16.5	16.5	16.4	16.2	16.2	16.1	16.1
574	524.5	481	478	447.5	430	420	419	409	400	319	302	273	272.5	265.5	264	263.5	263.5	258.5	257.5	257	257	256.5		253	252	251
13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

Search completed: May 18, 2004, 11:19:23 Job time : 11.613 secs

100.0 303 10 Q9MBE7 Q9mbe7 89.0 304 10 QELNZ1 C810Z1 C810Z1 C810Z1 C9mbe6 86.1 268 10 Q9MBE C9mbe6 Q9mbe7 82.7 306 10 Q88A58	1261 80.8 310 10 Q8S4C4 Q8S4C4 1232.5 79.0 306 10 O81845 O81845	1223.5 78.4 306 10 065623 065623 065623 1209.5 77.5 300 10 Q9AVG1 Q9avg1 1206.5 77.3 305 10 Q92WG1 Q92wg1 171 71.8 242 10 094FU6 094FU6	1112 71.2 241 10 1092 70.0 241 10 1091.5 69.9 286 10	1077.5 69.0 293 10 Q9AVG2 698.5 44.7 304 13 Q98T90 681.5 43.7 307 13 Q90T50 681.5 43.7 312 11 Q7INY4	680.5 43.6 309 11 Q9R246 Q9r246 Q9r246 680.5 43.6 309 11 Q8CBUO Q8cbuO 43.5 309 11 O9ER17 Q9er17 Q9er17	678.5 43.5 307 13 Q9DDT7 678.5 43.5 309 13 Q72V94 678.5 43.5 310 6 07XRE3	676.5 43.3 299 11 Q9ER16 675.5 43.3 307 13 QBAYM4 657.5 42.1 307 13 QZXN1 620 39.7 309 6 Q5GNZ1	30 618 39.6 273 6 09XSE1 099XSE2 Taurus 1818
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	Run on: May 18, 2004, 11:15:32 ; Search time 38.2067 Seconds (without alignments) 2502.235 Million cell updates/sec	Title: US-10-009-962-2 Perfect score: 1561 Sequence: 1 MGDHGPRTEISFAGSSRAAFVIMFLTLEQVKKFFIKEVPN 303	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 101/041 Seqs, 3.5510204 Testudes Total number of hits satisfying chosen parameters: 1017041	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SPTREMBL_25:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_lungi:* 4: sp_invertebrate:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mfo:* 8: sp_orderia:* 10: sp_plant:* 11: sp_volent:* 12: sp_virus:* 13: sp_vortebrate:* 14: sp_urclassified:* 14: sp_urclassified:* 15: sp_urclassified:* 16: sp_bacteriap:* 17: sp_archeap:* 18: sp_urclassified:* 19: sp_urclassified:* 10: sp_urclassified:* 11: sp_urclassified:* 12: sp_urclassified:* 13: sp_urclassified:* 14: sp_urclassified:* 15: sp_urclassified:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_urclassified:* 19: sp_urclassified:* 10: sp_urclassi

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241 SRMMGDSAYKSTFDCFIKTLKNDGLLAFYKGFIPNFGRLGSWNVIMFLTLEQVKKFFIKE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GPNIARNAIINAABLASYDQVKQTILKLPGFSDNIFTHILAGLGAGFFAVCIGSPVDVMK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGDHGPRTEISFAGSSRAAFAACFAELCTIPLDTAKVRLQLQKKAVTGDVVALPKYRGML 60
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Symplocarpus renifolius.
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
                                                                                                                                                                                                              Ito K.;
"Isolation of two distinct cold-inducible cDNAs encoding plant
uncoupling proteins from the spadix of skunk cabbage (Symplocarpus
                                                                                                                                                                                                                                                                                                       Toetidus)."

In Plant Sci. 149:167-173(1999).

- - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

REMBL, ABO24733 BAA92172.1, -

REGO; GO:00166021, C:integral to membrane; IEA.

RO; GO:0005743; C:mitochondrial inner membrane; IEA.

RO; GO:0005743; C:mitochondrial inner membrane; IEA.

RO; GO:0005488; F:binding, IEA.

RO; GO:0006488; F:binding, IEA.

RO; GO:0006489; P:mitochondrial transport; IEA.

RO; GO:0006499; P:mitochondrial transport; IEA.

RO; GO:0006499; P:mitochondrial transport; IEA.

RO; GO:0006819; P:mitochondrial transport; IEA.
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Job time : 40.2067 secs
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